

IN THE CLAIMS

3 – 14 (Cancelled)

15. (New) The method as claimed in claim 1, wherein the components of the mixed PCR product are digested with a restriction endonuclease before ligation to produce the concatenated sequence.

16. (New) The method as claimed in claim 1, wherein the concatenated sequence is cloned into a plasmid before sequencing.

17. (New) The method as claimed in claim 16, wherein the concatenated sequence is size selected to from about 500 to about 1.5 kilobases in length before cloning into the plasmid.

18. (New) The method as claimed in claim 2, wherein the length of each variable gene inserts is from about 18 to about 36 nucleotides.

19. (New) The method as claimed in claim 18, wherein the specific characteristic is one or more of protein binding or occurrence only in one state of tissue in a comparison with the same tissue in a different state.

20. (New) The method as claimed in claim 2, wherein the number of variable gene inserts are from phage which do not exhibit a specific characteristic.

21. (New) The method as claimed in claim 1, wherein selecting the number of inserts by their ability to exhibit the desired specific characteristic comprises two or more rounds of selection based on the ability of the variable gene inserts to exhibit the desired characteristic.

22. (New) The method as claimed in claim 1, wherein when more than one round of selection by the ability of the insert to exhibit the desired characteristic is carried out, then the different rounds of selection may be of more than one desired specific characteristic.
23. (New) The method as claimed in claim 1, further comprising characterisation of a target molecule.
24. (New) The method as claimed in claim 1, further comprising quantitation of a target molecule.
25. (New) The method as claimed in claim 23, wherein characterisation comprises using fluorescence resonant energy transfer.
26. (New) The method as claimed in claim 24, wherein quantitation comprises using fluorescence resonant energy transfer.
27. (New) A dataset of a sub-library resulting from the method of claim 1.
28. (New) A determination of the sequence or occurrence frequency of a number of variable gene inserts from a gene library obtained by the method of claim 1.